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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=2; day=5; hr=14; min=17; sec=45; ms=80; ]

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\*\*\*\*\*

Reviewer Comments:

<210> 7

<211> 54

<212> DNA

<213> Oligonucleotide Primer CF59

<400> 7

cgatagatct ttggataaga gagggccacc acctggcccc cctcgagttt cccc 54

The above <213> response is invalid, also similar responses were found in sequence id#'s 10 and 11. FYI, these responses can be inserted into section <220> to <223>.

\*\*\*\*\*

Application No: 10584438 Version No: 1.0

**Input Set:****Output Set:**

**Started:** 2008-01-29 15:17:14.169  
**Finished:** 2008-01-29 15:17:15.923  
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 754 ms  
**Total Warnings:** 20  
**Total Errors:** 1  
**No. of SeqIDs Defined:** 20  
**Actual SeqID Count:** 20

| Error code | Error Description  |
|------------|--|
| E 287      | Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <141> |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (1)       |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (2)       |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (3)       |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (4)       |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (5)       |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (6)       |
| W 402      | Undefined organism found in <213> in SEQ ID (7)          |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (8)       |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (9)       |
| W 402      | Undefined organism found in <213> in SEQ ID (10)         |
| W 402      | Undefined organism found in <213> in SEQ ID (11)         |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (12)      |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (13)      |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (14)      |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (15)      |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (16)      |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (17)      |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (18)      |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (19)      |

**Input Set:**

**Output Set:**

**Started:** 2008-01-29 15:17:14.169  
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**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 754 ms  
**Total Warnings:** 20  
**Total Errors:** 1  
**No. of SeqIDs Defined:** 20  
**Actual SeqID Count:** 20

| Error code | Error Description                                   |
|------------|---|
| W 213      | Artificial or Unknown found in <213> in SEQ ID (20) |

<210> 1  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Linker VC053  
  
 <400> 1  
 gatctttgga taagagagac gtcacaagt ccgaagtcgc tcaccggt 48  
  
 <210> 2  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Linker VC054  
  
 <400> 2  
 ccttgaaccg gtgagcgact tcggacttgt gagcgtctct cttatccaaa 50  
  
 <210> 3  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Linker VC055  
  
 <400> 3  
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 <210> 4  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Linker VC056  
  
 <400> 4  
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 <210> 5  
 <211> 86  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Linker VC057  
  
 <400> 5  
 tcaaggacct aggtgaggaa aacttcaagg ctttggtctt gatcgtttc gctcaatact 60  
 tgcaacaatg tccattcgaa gatcac 86  
  
 <210> 6

<211> 80  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotide Linker VC058  
  
 <400> 6  
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 gaagttttcc tcacctaggt 80

<210> 7  
 <211> 54  
 <212> DNA  
 <213> Oligonucleotide Primer CF59  
  
 <400> 7  
 cgatagatct ttggataaga gagggccacc acctggcccc cctcgagttt cccc 54

<210> 8  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Polypeptide linker SEQ ID 8  
  
 <400> 8  
 Gly Gly Gly Gly Ser  
 1 5

<210> 9  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Polypeptide linker SEQ ID 9  
  
 <400> 9  
 Gly Gly Gly Ser  
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<210> 10  
 <211> 17  
 <212> PRT  
 <213> Stanniocalcin signal peptide sequence  
  
 <400> 10  
 Met Leu Gln Asn Ser Ala Val Leu Leu Leu Val Ile Ser Ala Ser  
 1 5 10 15

Ala  
  
 <210> 11  
 <211> 22

<212> PRT  
<213> Consensus signal sequence

<400> 11  
Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Leu Ala Leu  
1 5 10 15  
  
Trp Ala Pro Ala Arg Gly  
20

<210> 12  
<211> 66  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide Primer CF60

<400> 12  
ggccatcgat gagcgacttc ggacttggtga gcgtccagcc gagtcttcag cagcagcagt 60  
cccttc 66

<210> 13  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide Primer CF61

<400> 13  
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<210> 14  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide Primer CF62

<400> 14  
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<210> 15  
<211> 2358  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> N-terminal IL11-albumin fusion

<400> 15  
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ctggacagca cgtgctcct gacctgctct ctctggcgg acacgcggca gctggctgca 180  
cagctgaggg acaaattccc agctgacggg gaccacaacc tggattccct gccaccctg 240

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gccatgagtgc cgggggcact gggagctcta cagctcccag gtgtgctgac aaggctgcga 300
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ccaaagtgg atgaattgag agacgaagggt aaggcttctt ccgctaagca aagattgaag 1200
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ttgtgtgttt tgcacgaaaa gaccccgctc tctgatagag tcaccaagtg ttgtactgaa 2040
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```

<210> 16
<211> 786
<212> PRT
<213> Artificial Sequence

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<220>
<223> N-terminal IL11-albumin fusion

```

```

<400> 16
Met Lys Trp Val Phe Ile Val Ser Ile Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Arg Ser Leu Asp Lys Arg Gly Pro Pro Pro Gly Pro Pro Arg
20 25 30

Val Ser Pro Asp Pro Arg Ala Glu Leu Asp Ser Thr Val Leu Leu Thr
35 40 45

Arg Ser Leu Leu Ala Asp Thr Arg Gln Leu Ala Ala Gln Leu Arg Asp
50 55 60

```

Lys Phe Pro Ala Asp Gly Asp His Asn Leu Asp Ser Leu Pro Thr Leu  
 65 70 75 80

Ala Met Ser Ala Gly Ala Leu Gly Ala Leu Gln Leu Pro Gly Val Leu  
 85 90 95

Thr Arg Leu Arg Ala Asp Leu Leu Ser Tyr Leu Arg His Val Gln Trp  
 100 105 110

Leu Arg Arg Ala Gly Gly Ser Ser Leu Lys Thr Leu Glu Pro Glu Leu  
 115 120 125

Gly Thr Leu Gln Ala Arg Leu Asp Arg Leu Leu Arg Arg Leu Gln Leu  
 130 135 140

Leu Met Ser Arg Leu Ala Leu Pro Gln Pro Pro Pro Asp Pro Pro Ala  
 145 150 155 160

Pro Pro Leu Ala Pro Pro Ser Ser Ala Trp Gly Gly Ile Arg Ala Ala  
 165 170 175

His Ala Ile Leu Gly Gly Leu His Leu Thr Leu Asp Trp Ala Val Arg  
 180 185 190

Gly Leu Leu Leu Leu Lys Thr Arg Leu Asp Ala His Lys Ser Glu Val  
 195 200 205

Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val  
 210 215 220

Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His  
 225 230 235 240

Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala  
 245 250 255

Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly  
 260 265 270

Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met  
 275 280 285

Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu  
 290 295 300

Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu  
 305 310 315 320

Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu  
 325 330 335

Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala  
 340 345 350

Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu  
 355 360 365

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Cys | Gln | Ala | Ala | Asp | Lys | Ala | Ala | Cys | Leu | Leu | Pro | Lys | Leu | Asp | 370 | 375 | 380 |     |
| Glu | Leu | Arg | Asp | Glu | Gly | Lys | Ala | Ser | Ser | Ala | Lys | Gln | Arg | Leu | Lys | 385 | 390 | 395 | 400 |
| Cys | Ala | Ser | Leu | Gln | Lys | Phe | Gly | Glu | Arg | Ala | Phe | Lys | Ala | Trp | Ala | 405 | 410 | 415 |     |
| Val | Ala | Arg | Leu | Ser | Gln | Arg | Phe | Pro | Lys | Ala | Glu | Phe | Ala | Glu | Val | 420 | 425 | 430 |     |
| Ser | Lys | Leu | Val | Thr | Asp | Leu | Thr | Lys | Val | His | Thr | Glu | Cys | Cys | His | 435 | 440 | 445 |     |
| Gly | Asp | Leu | Leu | Glu | Cys | Ala | Asp | Asp | Arg | Ala | Asp | Leu | Ala | Lys | Tyr | 450 | 455 | 460 |     |
| Ile | Cys | Glu | Asn | Gln | Asp | Ser | Ile | Ser | Ser | Lys | Leu | Lys | Glu | Cys | Cys | 465 | 470 | 475 | 480 |
| Glu | Lys | Pro | Leu | Leu | Glu | Lys | Ser | His | Cys | Ile | Ala | Glu | Val | Glu | Asn | 485 | 490 | 495 |     |
| Asp | Glu | Met | Pro | Ala | Asp | Leu | Pro | Ser | Leu | Ala | Ala | Asp | Phe | Val | Glu | 500 | 505 | 510 |     |
| Ser | Lys | Asp | Val | Cys | Lys | Asn | Tyr | Ala | Glu | Ala | Lys | Asp | Val | Phe | Leu | 515 | 520 | 525 |     |
| Gly | Met | Phe | Leu | Tyr | Glu | Tyr | Ala | Arg | Arg | His | Pro | Asp | Tyr | Ser | Val | 530 | 535 | 540 |     |
| Val | Leu | Leu | Leu | Arg | Leu | Ala | Lys | Thr | Tyr | Glu | Thr | Thr | Leu | Glu | Lys | 545 | 550 | 555 | 560 |
| Cys | Cys | Ala | Ala | Ala | Asp | Pro | His | Glu | Cys | Tyr | Ala | Lys | Val | Phe | Asp | 565 | 570 | 575 |     |
| Glu | Phe | Lys | Pro | Leu | Val | Glu | Glu | Pro | Gln | Asn | Leu | Ile | Lys | Gln | Asn | 580 | 585 | 590 |     |
| Cys | Glu | Leu | Phe | Glu | Gln | Leu | Gly | Glu | Tyr | Lys | Phe | Gln | Asn | Ala | Leu | 595 | 600 | 605 |     |
| Leu | Val | Arg | Tyr | Thr | Lys | Lys | Val | Pro | Gln | Val | Ser | Thr | Pro | Thr | Leu | 610 | 615 | 620 |     |
| Val | Glu | Val | Ser | Arg | Asn | Leu | Gly | Lys | Val | Gly | Ser | Lys | Cys | Cys | Lys | 625 | 630 | 635 | 640 |
| His | Pro | Glu | Ala | Lys | Arg | Met | Pro | Cys | Ala | Glu | Asp | Tyr | Leu | Ser | Val | 645 | 650 | 655 |     |
| Val | Leu | Asn | Gln | Leu | Cys | Val | Leu | His | Glu | Lys | Thr | Pro | Val | Ser | Asp | 660 | 665 | 670 |     |

Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys  
 675 680 685

Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn  
 690 695 700

Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys  
 705 710 715 720

Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His  
 725 730 735

Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe  
 740 745 750

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys  
 755 760 765

Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu  
 770 775 780

Gly Leu  
 785

<210> 17  
 <211> 762  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mature N-terminal IL11-albumin fusion

<400> 17

Gly Pro Pro Pro Gly Pro Pro Arg Val Ser Pro Asp Pro Arg Ala Glu  
 1 5 10 15

Leu Asp Ser Thr Val Leu Leu Thr Arg Ser Leu Leu Ala Asp Thr Arg  
 20 25 30

Gln Leu Ala Ala Gln Leu Arg Asp Lys Phe Pro Ala Asp Gly Asp His  
 35 40 45

Asn Leu Asp Ser Leu Pro Thr Leu Ala Met Ser Ala Gly Ala Leu Gly  
 50 55 60

Ala Leu Gln Leu Pro Gly Val Leu Thr Arg Leu Arg Ala Asp Leu Leu  
 65 70 75 80

Ser Tyr Leu Arg His Val Gln Trp Leu Arg Arg Ala Gly Gly Ser Ser  
 85 90 95

Leu Lys Thr Leu Glu Pro Glu Leu Gly Thr Leu Gln Ala Arg Leu Asp  
 100 105 110

Arg Leu Leu Arg Arg Leu Gln Leu Leu Met Ser Arg Leu Ala Leu Pro  
 115 120 125

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Pro | Pro | Pro | Asp | Pro | Pro | Ala | Pro | Pro | Leu | Ala | Pro | Pro | Ser | Ser | 130 | 135 | 140 |     |
| Ala | Trp | Gly | Gly | Ile | Arg | Ala | Ala | His | Ala | Ile | Leu | Gly | Gly | Leu | His | 145 | 150 | 155 | 160 |
| Leu | Thr | Leu | Asp | Trp | Ala | Val | Arg | Gly | Leu | Leu | Leu | Leu | Lys | Thr | Arg | 165 | 170 | 175 |     |
| Leu | Asp | Ala | His | Lys | Ser | Glu | Val | Ala | His | Arg | Phe | Lys | Asp | Leu | Gly | 180 | 185 | 190 |     |
| Glu | Glu | Asn | Phe | Lys | Ala | Leu | Val | Leu | Ile | Ala | Phe | Ala | Gln | Tyr | Leu | 195 | 200 | 205 |     |
| Gln | Gln | Cys | Pro | Phe | Glu | Asp | His | Val | Lys | Leu | Val | Asn | Glu | Val | Thr | 210 | 215 | 220 |     |
| Glu | Phe | Ala | Lys | Thr | Cys | Val | Ala | Asp | Glu | Ser | Ala | Glu | Asn | Cys | Asp | 225 | 230 | 235 | 240 |
| Lys | Ser | Leu | His | Thr | Leu | Phe | Gly | Asp | Lys | Leu | Cys | Thr | Val | Ala | Thr | 245 | 250 | 255 |     |
| Leu | Arg | Glu | Thr | Tyr | Gly | Glu | Met | Ala | Asp | Cys | Cys | Ala | Lys | Gln | Glu | 260 | 265 | 270 |     |
| Pro | Glu | Arg | Asn | Glu | Cys | Phe | Leu | Gln | His | Lys | Asp | Asp | Asn | Pro | Asn | 275 | 280 | 285 |     |
| Leu | Pro | Arg | Leu | Val | Arg | Pro | Glu | Val | Asp | Val | Met | Cys | Thr | Ala | Phe | 290 | 295 | 300 |     |
| His | Asp | Asn | Glu | Glu | Thr | Phe | Leu | Lys | Lys | Tyr | Leu | Tyr | Glu | Ile | Ala | 305 | 310 | 315 | 320 |
| Arg | Arg | His | Pro | Tyr | Phe | Tyr | Ala | Pro | Glu | Leu | Leu | Phe | Phe | Ala | Lys | 325 | 330 | 335 |     |
| Arg | Tyr | Lys | Ala | Ala | Phe | Thr | Glu | Cys | Cys | Gln | Ala | Ala | Asp | Lys | Ala | 340 | 345 | 350 |     |
| Ala | Cys | Leu | Leu | Pro | Lys | Leu | Asp | Glu | Leu | Arg | Asp | Glu | Gly | Lys | Ala | 355 | 360 | 365 |     |
| Ser | Ser | Ala | Lys | Gln | Arg | Leu | Lys | Cys | Ala | Ser | Leu | Gln | Lys | Phe | Gly | 370 | 375 | 380 |     |
| Glu | Arg | Ala | Phe | Lys | Ala | Trp | Ala | Val | Ala | Arg | Leu | Ser | Gln | Arg | Phe | 385 | 390 | 395 | 400 |
| Pro | Lys | Ala | Glu | Phe | Ala | Glu | Val | Ser | Lys | Leu | Val | Thr | Asp | Leu | Thr | 405 | 410 | 415 |     |
| Lys | Val | His | Thr | Glu | Cys | Cys | His | Gly | Asp | Leu | Leu | Glu | Cys | Ala | Asp | 420 | 425 | 430 |     |

Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile  
435 440 445

Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser  
450 455 460

His Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro  
465 470 475 480

Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr  
485 490 495

Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala  
500 505 510

Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys  
515 520 525

Thr Tyr Glu Thr Thr Leu Glu Lys Cys